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FIG. 1A

1	TGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGTTGGGGAGCC	60
61	TCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGATAGGGCGAGGCT	120
121	GTGCTGTCCTTTTCAGAAGACTTCCGGCGCACCATGGCATCCAGCATCCTCAAGTGGGTGG	180
1	M A S S I L K W V V	10
181	TCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGCAAGCCCAGGGACCAGAGGGAGGAGG	240
11	S H Q S C S R S S R S K P R D Q R E E A	30
241	CCGGGAGCAGCGACCTGAGCAGCAGGCAAGATGCTGAAAATGCTGAGGCAAAGCTCAGGG	300
31	G S S D L S S R Q D A E N A E A K L R G	50
301	GCCTCCCGGGGCGAGCTTGTGGACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGC	360
51	L P G Q L V D I A C K V C Q A Y L G Q L	70
361	TGGAGCATGAGGACATCGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGT	420
71	E H E D I D T S A D A V E D L T E A E W	90
421	GGGAGGACCTGACCCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATT	480
91	E D L T Q Q Y Y S L V H G D A F I S N S	110
481	CAAGAAATTACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTC	540
111	R N Y F S Q C Q A L L N R I T S V N P Q	130
541	AGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGG	600
131	T D I D G L R N I W I I K P A A K S R G	150
601	GCCGAGACATAGTGTGCATGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACC	660
151	R D I V M D R V E E I L E L A A A D H	170
661	ACCCTCTTTCCAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCA	720
171	P L S R D N K W V V Q K Y I E T P L L I	190
721	TCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCTGA	780
191	C D T K F D I R Q W F L V T D W N P L T	210
781	CCATCTGGTTCTACAAGGAGAGTTACTTGCGTTCTCAACTCAGCGCTTCTCCCTGGACA	840
211	I W F Y K E S Y L R F S T Q R F S L D K	230

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FIG. 1B

841	AGCTGGACAGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATG	900
231	<u>L D S A I H L [] N N A V Q K Y L K N D V</u>	250
901	TGGGCCGCGAGCCCCCTGCTGCCCCGACACAACATGTGGACCAGCACCAGGTTCCAGGAGT	960
251	<u>G R S P L L P A H N M W T S T R F Q E Y</u>	270
961	ACCTGCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGA	1020
271	<u>L Q R Q G R G A V W G S V I Y P S M K K</u>	290
1021	AGGCCATCGCCACGCCATGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCT	1080
291	<u>A I A H A M K V A Q D H V E P R K N S F</u>	310
1081	TTGAGCTCTACGGGGCTGACTTCGTCTTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGA	1140
311	<u>E L Y G A D F V L G R D F R P W L I E I</u>	330
1141	TCAATTCCAGCCCCACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGG	1200
331	<u>N S S P T M H P S T P V T A Q L [] A Q V</u>	350
1201	TGCAGGAGGACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGC	1260
351	<u>Q E D T I K V A V D R S [] D I G N F E L</u>	370
1261	TCCTGTGGAGGCAGCCGGTGGTTGAGCCGCCCCATTTCAGCGGGTCCGACCTCTGCGTGG	1320
371	<u>L W R Q P V V E P P P F S G S D L [] V A</u>	390
1321	CGGGCGTCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCCGTCTGCAACCTCAAGGCCT	1380
391	<u>G V S V R R A R R Q V L P V C N L K A S</u>	410
1381	CGGCCTCGTGTGTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCCTCGGCCATGCCAGACC	1440
411	<u>A S L L D A Q P L K A R G P S A M P D P</u>	430
1441	CTGCCCAGGGACCCCCATCACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGG	1500
431	<u>A Q G P P S P A L Q R D L G L K E E K G</u>	450
1501	GGCTCCCCCTGGCCTTGCTGGCACCCCTTAAGGGGGCAGCCGAGAGCGGTGGAGCCGCAC	1560
451	<u>L P L A L L A P L R G A A E S G G A A Q</u>	470
1561	AGCCCACCCGCACCAAAGCTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCCTGTCGCCACG	1620
471	<u>P T R T K A A G K V E L P A C P C R H V</u>	490
1621	TGGACAGTCAGGCCCCAAACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTGGGATC	1680
491	<u>D S Q A P N T G V P V A Q P A K S W D P</u>	510

FIG. 1C

1681	CAAACCAAGCTAAATGCGCACCCGCTGGAGCCTGTGCTGCGGGGCCTGAAGACAGCAGAGG	1740
511	N Q L N A H P L E P V L R G L K T A E G	530
1741	GCGCGCTGCGTCCGCCGCCCGGAGGAAAAGGTTTCATGACAGCGTCAGATTCTCTGCAGCA	1800
531	A L R P P P G G K G S	541
1801	GGAGTACAGGTTGCAGCCACTCTCCCAAGGGCGAATTC	1838

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FIG. 2

1	ATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGGGCGGAGAC	60
1	I D G L R N I W I I K P A A K S R G R D	20
61	ATAGTGTGCATGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACCACCTCTT	120
21	I V C M D R V E E I L E L A A A D H P L	40
121	TCCAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGAC	180
41	S R D N K W V V Q K Y I E T P L L I C D	60
181	ACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCTGACCATCTGG	240
61	T K F D I R Q W F L V T D W N P L T I W	80
241	TTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGAC	300
81	F Y K E S Y L R F S T Q R F S L D K L D	100
301	AGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGC	360
101	S A I H L C N N A V Q K Y L K N D V G R	120
361	AGCCCCCTGCTGCCCCGACACAACATGTGGACCAGCACCAGGTTCCAGGAGTACCTGCAG	420
121	S P L L P A H N M W T S T R F Q E Y L Q	140
421	CGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATC	480
141	R Q G R G A V W G S V I Y P S M K K A I	160
481	GCCCACGCCATGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTC	540
161	A H A M K V A Q D H V E P R K N S F E L	180
541	TACGGGGCTGACTTCGTCCCTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCC	600
181	Y G A D F V L G R D F R P W L I E I N S	200
601	AGCCCCACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAG	660
201	S P T M H P S T P V T A Q L C A Q V Q E	220
661	GACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGG	720
221	D T I K V A V D R S C D I G N F E L L W	240
721	AGGCAG	726
241	R Q	242

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FIG. 3A

		1		50
BGS-42	(1)	-----MASSILKWVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAE		
TTL_PIG	(1)	MYTFVVRDENS SVYAEVSRLLLATGHWKRLRRDNPRFNLMLGERNRLPFG		
TTLH_Hu	(1)	-----MAGKVKWVTDIEKSVLINNFEKRGWVQVTENEDWNFYWMSV		
HOTTTL	(1)	-----		
		51		100
BGS-42	(43)	NAEAKLRGLPGQLVDIACKVCQAYLGQLEHEDIDTSADAVEDLTAEWED		
TTL_PIG	(51)	RLGHEPGLMQLVNYYRGADKLCKASLVKLIKTSPELAESCTWFPESYVI		
TTLH_Hu	(42)	QTIRNVFSVEAGYRLSDDQIVNHFP--NHVELTRKQIMVKN--IKRYRKE		
HOTTTL	(1)	-----MDIDKQLEAPLYLTPEGWSL		
		101		150
BGS-42	(93)	LTQQYYSLVHGDAFISNSRNYFSQCQALLNRIITSVNPQTDIDGLRNIIWII		
TTL_PIG	(101)	YPTNLKTPVAPAQNGIHPPIHSSRTDEREFFLTSYNKKKE-DGEGNVWIA		
TTLH_Hu	(88)	LEKEGSPLAEKDENGKYLDFVPVTYMLPADYNLFVEEFRKSPSSTWIM		
HOTTTL	(1)	-----MEGDRNFWIV		
		151		200
BGS-42	(143)	KPAAKSRGRDIVCMRVEETLELAAADHPISRDN-----KWVVQKYIETP		
TTL_PIG	(150)	KSSAGAKGEGILISSEATELDFIDN-----OGQ-----VHVIQKYLERP		
TTLH_Hu	(138)	KPCCKAQCCKGIFLTKLSQTKKWSRDSKTSSFVSQSNKEAYVISLYINNP		
HOTTTL	(11)	KPCAASRGIMCMDHLEEMKLIVNGNPVVMKDG-----KWVVQKYIERP		
		201		250
BGS-42	(188)	LLICD--TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSA-		
TTL_PIG	(190)	LLLEPGHRKFDIRSWVLVD--HQYNIYLYREGVLRASEPYHTDNFQDKT		
TTLH_Hu	(188)	LLIGG--RKFDLRLLVVLVSTYRPLRCYMYKLGFRCFCTVKYTPSTISELDN		
HOTTTL	(56)	LLIFG--TKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNS-		
		251		300
BGS-42	(235)	--IHLCNNAVOKYLLKNDVGRSPLLPAHNMWTSTRFOEYLRQCRGAVWGS		
TTL_PIG	(238)	--CHLTNHCIQKEYSKNYGKYE--E-GNEMFFEEFNQYLTSAL-NITLES		
TTLH_Hu	(236)	MFVHLTNVAIQKHGEDYNHIIH---G--GKWTIVSNLRLYLESTR-GKEVTS		
HOTTTL	(103)	--VHLCNNSIQKHLENSCHRHPLLEPDNMWSSORFOAHLQEMCAPNAWST		
		301		350
BGS-42	(283)	VIYPSMKKATAHAMKVAODHVEPRKN---SFELYGADFVLGRDFRPWLEIE		
TTL_PIG	(282)	SILLQIKHIIRSCLLSVEPAISTRHLPYQSFQLFGFDFMVDEDLKQVWLEIE		
TTLH_Hu	(280)	KLFDEIHWIIVQSLKAVAPVMNNDKH---CFECYGYDIIIDDKLKPWLEIE		
HOTTTL	(151)	IIVPGMKDAVIHALQTSQDTVQCRKA---SFELYGADFVFGEDFQPWLEIE		

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FIG. 3B

		351		400
BGS-42	(330)	INSSPTMHPSTPVTACOLCAQVQEDTIKVAVD	-----	RSCDIG
TTL_PIG	(332)	VNG-----APACAOKLYAELCOGIVDIAIAS	-----	
TTLH_Hu	(327)	VNASPSLTSSSTANDRILKYNTLINDTLNIAVPNGEIPDCKWNKSPPEVLG		
TTLH_Hu	(258)	INASPTMAPSTAVTARLCAGVQADTLRVVIDR	-----	MLDRNCDTG
HOTTTL	(198)	INASPTMAPSTAVTARLCAGVQADTLRVVIDR	-----	MLDRNCDTG
		401		450
BGS-42	(367)	NFELLWRQPVEPPPFSGSDLGVAGVSVRRARRQVLPVCNLKASASLLDA		
TTL_PIG	(358)	VFPPPDAAEQQQQ-----QPPPAAFIKL	-----	
TTLH_Hu	(377)	NYEILYDEELAQGDGADRELRSRQGSLGPFRAGR	-----	SRDSGRAVLTT
TTLH_Hu	(299)	AFELIYKQPVTTSFASTPRPSCLLPMYSDTRAR	-----	SSDDSTASW
HOTTTL	(239)	AFELIYKQPVTTSFASTPRPSCLLPMYSDTRAR	-----	SSDDSTASW
		451		500
BGS-42	(417)	QPLKARGPSAMPDPAQGPPSPALQRDGLKEEKGLPLALLAPLRGA AESG		
TTL_PIG	(380)	-----	-----	
TTLH_Hu	(422)	WK-----	-----	
TTLH_Hu	(341)	WALRPCRPOARP	-----	
HOTTTL	(281)	WALRPCRPOARP	-----	
		501		550
BGS-42	(467)	GAAQPTRTKAAGKVELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAH		
TTL_PIG	(380)	-----	-----	
TTLH_Hu	(424)	-----	-----	
TTLH_Hu	(353)	-----	-----	
HOTTTL	(293)	-----	-----	
		551		575
BGS-42	(517)	PLEPVLRGLKTAEGALRPPPGGKGS		
TTL_PIG	(380)	-----	-----	
TTLH_Hu	(424)	-----	-----	
TTLH_Hu	(353)	-----	-----	
HOTTTL	(293)	-----	-----	

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FIG. 4

Model	Description	Score	E-value	N
-----	-----	-----	-----	---
TTL	Tubulin-tyrosine ligase family	293.0	3.7e-84	1
Q	73 EDIDTS----ADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSR-----NYFSQCQALL ++ID + ' +++ ++ + W ++ ++ ++ + + ++ +++++			
T	1 MRIDMHYRMMHQMINHFPGSYWITRKDRLWMNIKRMMCDFHWKHDHFDWMPRTFILPTDY			
Q	122 NRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMRDVEEILELAA-----ADHPLSRDN +++ + ++ + +G++N+WI+KP++++RGR+I++M+ ++I+ ++ +P++ ++			
T	61 QEFVDYWQKHEWWGQDNHWIVKPWNSCRGRGIWIMNDWKQIPRWVNDFMDNPFVPPHQHRR			
Q	177 KWVVQKYIETPLLICD-----TKFDIRQWFLVTDWNPLTIWIFYKESYLRFSTQRF--LD +WVVQKYIE PLII +KFDIR+++LVT++NPL+I++Y+E+++RF+++ ++ +			
T	121 PWVVQKYIERPLIDGMDVGHHKFDIRCYVLVTSFNPLRIYVYREGWCRFCVVKYHPMDN			
Q	230 KLDSAIHLCNNAVQKYLKN--DVGRSPLLPAHNMTSTRFQEYLQR--QGRGAVWGSVIY + +HL+N+++QK+ +N +R +++++ ++MWT +F++Y+++ + ++W +++			
T	181 FDNYSMHLTNYCIQKHYSNYSRCNRDYNCHGHMWTLQNFWNYYENMGIDWDNIWSQICD			
Q	286 PSMKKAIAHA-MKVAQDHVEPRKNSFELYGADFVL---GRDFRPWLIEINSSPTMHPST + +K+++A++ +++++++PR+N+FELYG+DF + +++ PWL+E+N+SP+MH+++			
T	241 IIIKTIVAAWCVEACRMNQPRYNCFELYGFDFMIQWDDDENLKPWLLEVNWSPPMHCTC			
Q	341 PVTAQLCAQVQEDTIK-----VAVDRSCDI P+++ LC+Q+++D+++ V +D++ D+			
T	301 PYDMHLCHQLIRDVLNCAGCHVPPDCMKDC			

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FIG. 5A

BGS-42 – Clone A

TGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGTTGG
GGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGAT
AGGGCGAGGCTGTGCTGTCCTTTCAGAAGACTTCCGGCGCACCATGGCATCCAGC
ATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGCAAG
CCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGCAAGA
TGCTGAAAATGCTGAGGCAAAGCTCAGGGGGCCTCCCGGGGCAGCTTGTGGACAT
CGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACATCGA
CACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCTGAC
CCAGCAGTACTACTCCCTCGTTTCATGGCGATGCTTTCATCTCCAATTCAAGAAATT
ACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTCAGAC
GGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCG
GGGCCGAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTC
ATCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACC
CCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTT
CTCCCTGGACAAGCTGGACAGCGCCATCCACCTGTGCAACAACACCGTCCAGAA
GTACCTGAAGAATGATGTGGGCCGAGCCCCCTGCTGCCCCGACACAACATGTG
GACCAGCACCAGGTTCCAGGAGTACCTGCAGCGCCAGGGCCGTGGCGCCGTGTG
GGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATCGCCACGCCATGAAGGT
GGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTGA
CTTCGTCTTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCC
ACCATGCACCCGTCCACGCCGGTACGGCCCAGCTGTGTGCACAGGTGCAGGAG
GACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTC
CTGTGGAGGCAGCCGGTGGTTGAGCCGCCCCCATTCAGCGGGTCCGACCTCTGCG
TGGCGGGCGTCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACC
TCAAGGCCTCGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCCT
CGGCCATGCCAGACCCTGCCAGGGACCCCCATCACCAGCTCTCCAGCGGGACTT
GGGACTGAAGGAAGAGAAGGGGCTCCCCCTGGCCTTGCTGGCACCCCTTAAGGGG
GGCAGCCGAGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAGCTGCTGGGAA
GGTGGAGCTCCCGGCCTGCCCCTGTCGCCACGTGGACAGTCAGGCCCCAAACAC
CGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGA
GCACCCGCTGGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCG
TCCGCCGCCCCGAGGAAAAGGTTTCATGACAGCGTCAGATTCTCTGCAGCAGGAG
TACAGGTTGCAGCCACTCTCCCGCCGAACATTGAATACGTCTTCCACCATCTTGT
CTTTGCTGTGGCTCTGGGAAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAG
CTGTCAGTTCTATCTGCCAGCTTTTGAGTGTTCATTTGATTTTTACTTATTCAACC
TGGAATTTGAATGTCAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:9)

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FIG. 5B

BGS-42 – Clone B

GTAGCAGCGTG GGAAGAAGGAGTTCCTGGAAGACTTCCGGCGCACCATGGCATC
CAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAG
CAAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGC
AAGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGG
ACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACA
TCGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACC
TGACCCAGCAGTACTACTCCCTCGTTCATGCCAGGCTCTGCTGAATAGAATCACG
TCTGTGAACCCTCAGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGC
CCGCGGCCAAGTCCCGGGGCCGAGACATAGTGTGCATGGACCGTGTGGAGGAGA
TCCTGGAGCTGGCAGCTGCAGACCACCCTCTTTCCAGGGACAACAAGTGGGTGGT
CCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGACACCAAGTTCGACATCAG
ACAGTGGTTTCCTCGTCACGGACTGGAACCCCTGACCATCTGGTTCTACAAGGAG
AGTTACTTGC GGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGCGCCA
TCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGCA
GCCCCCTGCTGCCCCGCACACAACATGTGGACCAGCACCAAGTTCCAGGAGTACCT
GCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAA
GAAGGCCATCGCCACGCCATGAAGGTGGCCAGGACCACGTGGAGCCTCGCAA
GAACAGCTTTGAGCTCTACGGGGCTGACTTCGTCTTGGGAGGGACTTCAGGCCC
TGGCTGATCGAGATCAATTCCAGCCCCACCATGCACCCGTCCACGCCGGTCACGG
CCCAGCTGTGTGCACAGGTGCAGGAGGACACCATCAAGGTGGCCGTGGACCGCA
GCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGCCGGTGGTTGAGCCGCCCCCA
TTCAGCGGGTCCGACCTCTGCGTGGCGGGCGTCAGTGTGAGGAGAGCCAGGAGG
CAGGTGCTGCCCCGTCTGCAACCTCAAGGCCTCGGCCTCGCTGTTGGACGCGCAGC
CGCTGAAGGCACGGGGCCCCCTCGGCCATGCCAGACCCTGCCAGGGACCCCCAT
CACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGGGGCTCCCCCTGG
CCTTGCTGGCACCTTAAGGGGGGCAGCCGAGAGCGGTGGAGCCGCACAGCCCA
CCCGCACCAAAGCTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCTGTGCGCCACGT
GGACAGTCAGGCCCCAAACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTG
GGATCCAAACCAGCTAAATGAGCACCCGCTGGAGCCTGTGCTGCGGAGCCTGAA
GACAGCAGAGGGCGCGCTGCGTCCGCCGCCCGGAGGAAAAGGTTTCATGACAGCG
TCAGATTCTCTGCAGCAGGAGTACAGGTTGCAGCCACTCTCCCGCCGAACATTGA
ATACGTCTTTCCACCATCTTGTCTTTGCTGTGGCTCTGGGAAAATCAGCAGAGTC
AGCCATCACTCTCCAAGGGGAGCTGTGAGTTCTATCTGCCAGCTTTTGAGTGTTC
AATTTGATTTTTACTTATTCAACCTGGAATTTGAATGTCAAAAAAAAAAAAAAAAAA
AAAAAAAAA (SEQ ID NO:10)

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FIG. 5C

BGS-42 – Clone C

CCCAGGACTCCTGGTCTAAGGCCGTGGCCAGAATCACTCGGTGCCCACCCACCC
CCAGCACCCCTGTGCCCTTTGCTCTGTGTCTCTGGGTGAATCCGGGGGCCCCAGAA
GCTCCCTCCTCAGGGCACAGAGGCCAAAGATGGGGCTGACTGGGGGCTGCCACC
GGGCTTTGGGTGCTGAGGGGGCTGTGGGACCCAGGGGAAGAGGTGCCGCTCCC
CCCAGCACCGGGCACTCCCCCGCCTCCCCGGCCTCCAGCCCTGCACAAAGCAGC
TTGCCACACCCTTCCCACCAAGGCCAGGGCTGAGGCCTGCCAGGACGCAGGG
TGTGGGGACCCTGCTGAGGGAGGGGTCCCGGAAGAGGGGCTTCCCTGGCACAGA
GGTCCCTCTCAGCAGGCCAGGTGCGGCTGCCTCAGCACAGTGTGGGGCGGAGGT
GCAGGACAAGGTTCCCTTCCGCACCTAATACCCAGGGTCAGGCCAGCGCCAGC
GCTGCTAGTGGCAACATGGCCCCTTCAAAGACCCCGTGTGCAGAGCCAGTCAGC
GTGCGCTGTGTTTTCTGGGGGGCCAGCCACTTTTTTCTTAACGGGGTGACAAACC
AGACATCGGGGTGCGGGGACTTCACGATATGCCTCTCTAATGGCGCGTGCTACCT
CGCGTGTGGTGGGCAGTGCTGGGCATGTGGCTGCGTTCCGGGGCCCTGCAGCCGCT
CCTCCCTCTCCTGGGGTCTGAGGTGTGGGACACCCTGTGGCCCGTTTGGGGGCGCT
GGAGGGAGCCCCAGTGCCCAACGCCCTCGGTGCCCTCAGCTGCAGCCTCCCCATT
CCCTGGGGCCTGCCACGCCCTCCACTGCCTCAAGGATGCGTCTGAGCCTGGCCTG
CACATCCATGCTCCCACCGGCTGGAGGGGGTGTTCTGGGGCCCTGGGGGACCGT
ATATCTGGGGAGGGGGAGGGATCCGCCCTAGGGGTGCTGTGTGGTGCCCCATAG
CCAGGCAAGTCTGAGGTGGACGGCCCGTCCTCGCCTTGTGAGCGAGGCAGAGCT
GAGCTGAGCTGCCCCCTCCTGCCTAACACGCCACTGTCTCTGGAGATCGGGCTGTG
CGTGAACATGCGGAGCCTGCCCTGGTACGTCCCGGCCAACCCCGACTCCTTCTTC
CCACGCTGCTACAGCCTCTGCACCGAGAGTGAGCAGCAGGAGTTCCTGGGTAAG
TGAGGAGACGGCAGAGGGGCCCCAGTGCTGTCAGCAGAGAGGCTTCTAGAAAGAT
CCCCCTGGTGCTGAGACAGACTGATGGGGCAGGGTCTGAGGATAGAGGACCGGG
GAGAGGCCTCCCATGGTCATGGTCATGGCAGTACAGAGGCCAGGGGCCCCGGGA
GGGAGGGCGGGCAGTCAAGGAGTGTGTGGTTCTGTGCTAGGCTTGTGGACAGCG
CGGCGAGCAGCTGGGGCAAGGCCGGCTCCGTGGTTCGGAGGCCGAGGGGTGCAGC
TGGACGGCCGAGTACAGAGACACTGCAGGGAGAAGGGCAGGCAGACTGGGG
GTGTGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGT
TGGGGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCTTGGCTCGGACA
GATAGGGCGAGGCTGTGCTGTCCTTTCAGAAGACTTCCGGCGCACCATGGCATCC
AGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGC
AAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGCA
AGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGA
CATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACAT
CGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCT
GACCCAGCAGTACTACTCCCTCGTTTCATGGCGATGCTTTCATCTCCAATTCAAGA
AATTACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTC
AGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGT
CCCGGGGCGGAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCT
GCTCATCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGG
AACCCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGC
GCTTCTCCCTGGACAAG

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FIG. 5C (CONT.)

CTGGACAGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAA
GAATGATGTGGGCCGAGCCCCCTGCTGCCCCGACACAACATGTGGACCAGCAC
CAGGTTCCAGGAGTACCTGCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGT
CATCTACCCGTCCATGAAGAAGGCCATCGCCACGCCATGAAGGTGGCCCAGGA
CCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTGACTTCGTCCTT
GGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCATGCAC
CCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAGGACACCATC
AAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGG
CAGCCGGTGGTTGAGCCGCCCCCATTACAGCGGGTCCGACCTCTGCGTGGCGGGCG
TCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACCTCAAGGCCT
CGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCCTCGGCCATGC
CAGACCCTGCCCAGGGACCCCCATCACCAGCTCTCCAGCGGGACTTGGGACTGA
AGGAAGAGAAGGGGGCTCCCCCTGGCCTTGCTGGCACCCCTTAAGGGGGGCAGCCG
AGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAGCTGCTGGGAAGGTGGAGC
TCCCGGCCTGCCCCCTGTCGCCACGTGGACAGTCAGGCCCCAAACACCGGTGTCCC
CGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGAGCACCCGCT
GGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCGTCCGCCGCC
CGGAGGAAAAGGTTTCATGACAGCGTCAGATTCTCTGCAGCAGGAGTACAGGTTG
CAGCCACTCTCCCGCCGAACATTGAATACGTCTTTCCACCATCTTGTCTTTGCTGT
GGCTCTGGGAAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAGCTGTCAGT
TCTATCTGCCAGCTTTTGAGTGTTCATTTGATTTTACTTATTCAACCTGGAATTT
GAATGTCAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:11)

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FIG. 6A

1 GTCTAAGGCCGTGGCCAGAATCACTCGGTGCCCACCCACCCACAGCACCCCTGTGCCCT 60

61 TTGCTCTGTGTCTCTGGGTGAATCCGGGGCCCCAGAAGCTCCCTCCTCAGGGCACAGAGG 120

121 CCAAAGATGGGGCTGACTGGGGGCTGCCACCGGGCTTTGGGTGCTGAGGGGGCTGTGGGA 180

181 CCCCAGGGGAAGAGGTGCCGCTCCCCCAGCACCGGGCACTCCCCCGCTCCCCCGGCCT 240

241 CCAGCCCTGCACAAAGCAGCTTGCCACACCCTTCCCACCAAGGCCAGGGCTGAGGCCTG 300

301 CCCAGGACGCAGGGTGTGGGGACCCTGCTGAGGGAGGGGTCCCGGAAGAGGGGCTTCCCT 360

361 GGCACAGAGGTCCCTCTCAGCAGGCCAGGTGCGGCTGCCTCAGCACAGTGTGGGGCGGAG 420

421 GTGCAGGACAAGGTTCCCTTCCGCACCTAATAACCCAGGGTCAGGCCAGCGCCAGCGCTG 480

481 CTAGTGGCAACATGGCCCCTTCAAAGACCCCGTGTGCAGAGCCAGTCAGCGTGCGCTGTG 540

541 TTTTCTGGGGGCCAGCCACTTTTTTCTTAACGGGGTGACAAACCAGACATCGGGGTGCG 600

601 GGGACTTCACGATATGCCTCTCTAATGGCGCGTGCTACCTCGCGTGTGGTGGGCAGTGCT 660

661 GGGCATGTGGCTGCGTTCGGGGCCCTGCAGCCGCTCCTCCCTCTCCTGGGGTCTGAGGTG 720

721 TGGGACACCCTGTGGCCCGTTTGGGGGCTGGAGGGAGCCCCAGTGCCACCGCCCTCGG 780

781 TGCCCTCAGCTGCAGCCTCCCCATTCCCTGGGGCCTGCCACGCCCTCCACTGCCTCAAGG 840

841 ATGCGTCTGAGCCTGGCCTGCACATCCATGCTCCCACCGGCTGGAGGGGGTGTCTGGGG 900

901 CCCTGGGGGACCGTATATCTGGGGAGGGGGAGGGATCCGCCCTAGGGGTGCTGTGTGGTG 960

961 CCCCATAGCCAGGCAAGTCTGAGGTGGACGGCCCGTCCTCGCCTTGTGAGCGAGGCAGAG 1020

1021 CTGAGCTGAGCTGCCCCCTCCTGCCTAACACGCCACTGTCTCTGGAGATCGGGCTGTGCGT 1080

1081 GAACATGCGGAGCCTGCCCTGGTACGTCCCGGCCAACCCCGACTCCTTCTTCCCACGCTG 1140

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FIG. 6B

1141	CTACAGCCTCTGCACCGAGAGTGAGCAGCAGGAGTTCCTGGGTAAGTGAGGAGACGGCAG	1200
1201	AGGGCCCCAGTGCTGTCAGCAGAGAGGCTTCTAGAAAGATCCCCCTGGTGCTGAGACAGA	1260
1261	CTGATGGGGCAGGGTCTGAGGATAGAGGACCGGGGAGAGGCCTCCCATGGTCATGGTCAT	1320
1321	GGCAGTACAGAGGCCAGGGGCCCCGGGAGGGAGGGCGGGCAGTCAAGGAGTGTGTGGTTTC	1380
1381	TGTGCTAGGCTTGTGGACAGCGCGGCGAGCAGCTGGGGCAAGGCCGGCTCCGTGGTCGGA	1440
1441	GGCCGAGGGGTGCAGCTGGACGGCCGCAGTCACAGAGACACTGCAGGGAGAAGGGCAGGC	1500
1501	AGACTGGGGGTGTGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCG	1560
1561	GGTTGGGGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGA	1620
1621	TAGGGCGAGGCTGTGCTGTCCTTTTCAGAGTAGCAGCGTGGGAAGAAGGAGTTCCTGGAAG	1680
1681	ACTTCCGGCGCACCATGGCATCCAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCA	1740
1	M A S S I L K W V V S H Q S C S	16
1741	GCAGGAGCAGCAGAAGCAAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGA	1800
17	R S S R S K P R D Q R E E A G S S D L S	36
1801	GCAGCAGGCAAGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTG	1860
37	S R Q D A E N A E A K L R G L P G Q L V	56
1861	TGGACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACATCG	1920
57	D I A C K V C Q A Y L G Q L E H E D I D	76
1921	ACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCTGACCCAGC	1980
77	T S A D A V E D L T E A E W E D L T Q Q	96
1981	AGTACTACTCCCTCGTTTCATGGCGATGCTTTTCATCTCCAATTCAAGAAATTACTTTTCGC	2040
97	Y Y S L V H G D A F I S N S R N Y F S Q	116
2041	AGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTCAGACGGACATTGACGGGC	2100
117	C Q A L L N R I T S V N P Q T D I D G L	136

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FIG. 6C

2101	TCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGGGCGGAGACATAGTGTGCA	2160
137	R N I W I I K P A A K S R G R D I V C M	156
2161	TGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACCACCCTCTTTCCAGGGACA	2220
157	D R V E E I L E L A A A D H P L S R D N	176
2221	ACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGACACCAAGTTCTG	2280
177	K W V V Q K Y I E T P L L I C D T K F D	196
2281	ACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCTGACCATCTGGTTCTACAAGG	2340
197	I R Q W F L V T D W N P L T I W F Y K E	216
2341	AGAGTTACTTGC GTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGCGCCATCC	2400
217	S Y L R F S T Q R F S L D K L D S A I H	236
2401	ACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGAGCCCCCTGC	2460
237	L C N N A V Q K Y L K N D V G R S P L L	256
2461	TGCCCCGACACAACATGTGGACCAGCACCAGGTTCCAGGAGTACCTGCAGCGCCAGGGCC	2520
257	P A H N M W T S T R F Q E Y L Q R Q G R	276
2521	GTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATCGCCCACGCCA	2580
277	G A V W G S V I Y P S M K K A I A H A M	296
2581	TGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTG	2640
297	K V A Q D H V E P R K N S F E L Y G A D	316
2641	ACTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCA	2700
317	F V L G R D F R P W L I E I N S S P T M	336
2701	TGCACCCGTCCACGCCGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAGGACACCATCA	2760
337	H P S T P V T A Q L C A Q V Q E D T I K	356
2761	AGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGGCAGCCGG	2820
357	V A V D R S C D I G N F E L L W R Q P V	376
2821	TGGTTGAGCCGCCCCATTTCAGCGGGTCCGACCTCTGCGTGGCGGGCGTCAGTGTGAGGA	2880
377	V E P P P F S G S D L C V A G V S V R R	396
2881	GAGCCAGGAGGCAGGTGCTGCCCCTCTGCAACCTCAAGGCCTCGGCCTCGCTGTTGGACG	2940
397	A R R Q V L P V C N L K A S A S L L D A	416

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FIG. 6D

2941	CGCAGCCGCTGAAGGCACGGGGCCCCCTCGGCCATGCCAGACCCTGCCCAGGGACCCCCAT	3000
417	Q P L K A R G P S A M P D P A Q G P P S	436
3001	CACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGGGGCTCCCCCTGGCCTTGC	3060
437	P A L Q R D L G L K E E K G L P L A L L	456
3061	TGGCACCCCTTAAGGGGGGCAGCCGAGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAG	3120
457	A P L R G A A E S G G A A Q P T R T K A	476
3121	CTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCCTGTGCGCCACGTGGACAGTCAGGCCCCAA	3180
477	A G K V E L P A C P C R H V D S Q A P N	496
3181	ACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGAGC	3240
497	T G V P V A Q P A K S W D P N Q L N E H	516
3241	ACCCGCTGGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCGTCCGCCGC	3300
517	P L E P V L R S L K T A E G A L R P P P	536
3301	CCGGAGGAAAAGGTTTCATGACAGCGTCAGATTCTCTGCAGCAGGAGTACAGGTTGCAGCC	3360
537	G G K G S	541
3361	ACTCTCCCGCCGAACATTGAATACGTCTTTCCACCATCTTGTCTTTGCTGTGGCTCTGGG	3420
3421	AAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAGCTGTCAGTTCTATCTGCCAGCTT	3480
3481	TTGAGTGTTCAATTTGATTTTTTACTTATTCAACCTGGAATTTGAATGTCAAAAAAAAAA	3540
3541	AAAAAAAAAAAAA	3554

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FIG. 7A

-2057 tgcctgcagcagagcccggctgggatacctcacgctgcacgccatttgcctctgatggtt -1998

-1997 gcctcactccatcccatcctggctggtgtgaaccttgaatgctgggcatcaataaagact -1938

-1937 tttttcttgccagtctaggttggtaaaaaatgagatgccgtacctcctctggaccatcaa -1878

-1877 gaaggacatcattgactatcacagcctgacctacgaccagatgctgaaccactacgcaaa -1818

-1817 gacagcctccttcaccaccaaggtgagccggccgccttgagcgtggcgggagccggcaa -1758

-1757 gggtggtggggaggagcttctgcagccattagggaccctcggtggctggtcagtggccac -1698

-1697 cagtcacctcctgggtgcatcccaggactcctggtctaaggccgtggccagaatcactcg -1638

-1637 gtgcccacccccccccagcaccctgtgccctttgctctgtgtctctgggtgaatccgg -1578

-1577 ggccccagaagctccctcctcagggcacagaggccaaagatggggctgactgggggctgc -1518

-1517 caccgggctttgggtgctgagggggctgtgggacccccaggggaagaggtgccgctcccc -1458

-1457 cagcaccgggactccccgcctccccggcctccagccctgcacaaagcagcttgccac -1398

-1397 acccttcccaccaaggcccagggtgagggcctgccaggacgcagggtgtggggaccctg -1338

-1337 ctgaggagggggtcccggaagaggggcttccctggcacagaggtccctctcagcaggcca -1278

-1277 ggtgcggtgcctcagcacagtgtggggcggaggtgcaggacaaggttcccttccgcacc -1218

-1217 taataccccagggtcaggccagcgcacgcctgctagtggcaacatggccccttcaaaga -1158

-1157 ccccgtgtgcagagccagtcaacgtgcctgtgttttctgggggcccagccactttttcc -1098

-1097 ttaacaggggtgacaaaccagacatcgggggtgcggggacttcacgatatgcctctctaag -1038

-1037 gcgcgtgctacctcgcctgtggtgggcagtgctgggcacatgtgctgccttccgggcccctg -978

-977 caqccgctcctccctctcctggggtctgaggtgtgggacaccctgtggcccgtttggggg -918

-917 cctggaggggagccccagtgcccaccgcccctcggtgccctcagctgcagcctccccattcc -858

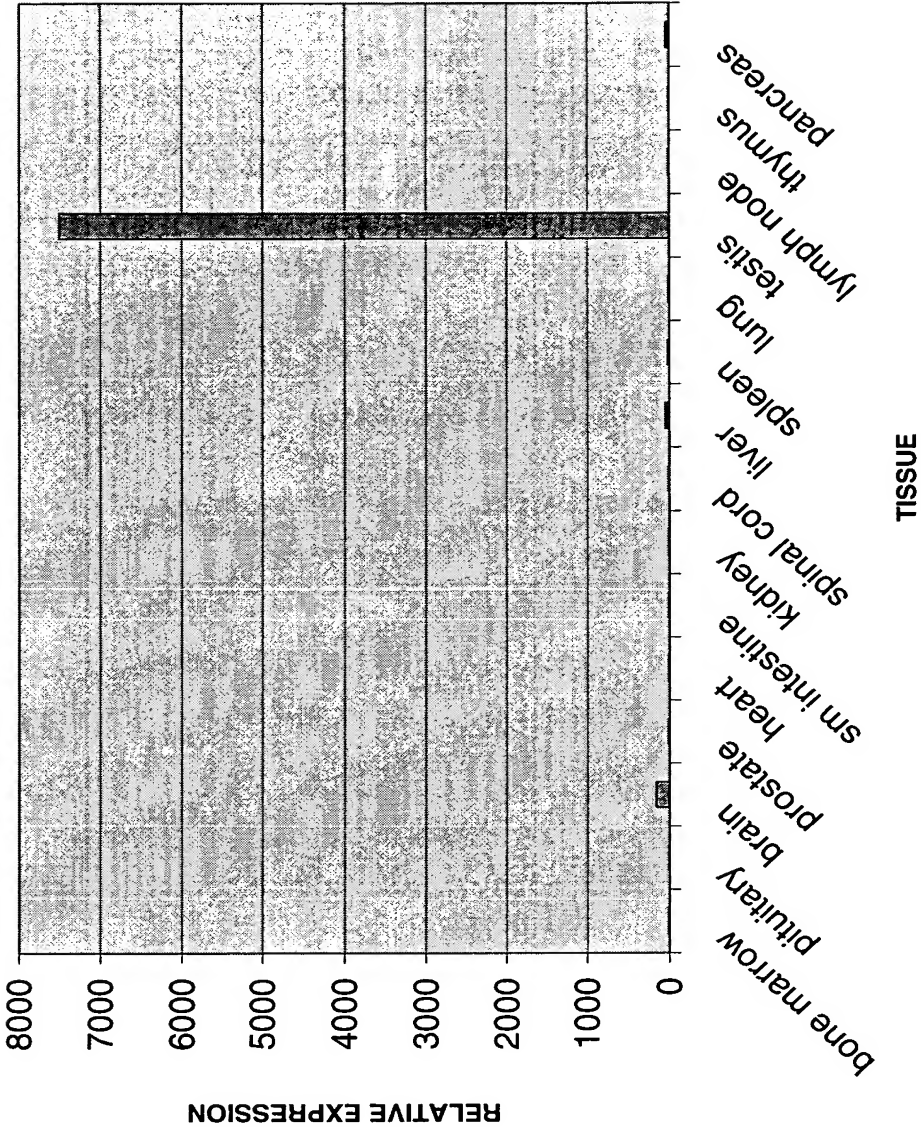
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FIG. 7B

-857	ctggggcctgccacgccctccactgcctcaaggatgCGTctgagcctggcctgcacatcc	-798
-797	atgctcccaccggctggaggggtgttctggggccctgggggaccgtatatctggggagg	-738
-737	gggagggatccgccctaggggtgctgtgtggtgccccataqccaggcaagtctgaggtgg	-678
-677	<u>acggccctcctcgccctgtgagcgaggcagagctgagctgagctgccccctcctgcctaa</u>	-618
-617	<u>cacgccactgtctctggagatcgggctgtgcctgaacatcgggagcctgccctggtacgt</u>	-558
-557	<u>cccggccaaccccgaactccttcttcccacgctgctacagcctctgcaccgagagtgaagca</u>	-498
-497	<u>gcaggagttcctgggtaaagtgaggagacggcagagggccccagtgctgtcagcagagagg</u>	-438
-437	cttctagaaagatccccctggtgctgagacagactgatggggcagggtctgaggatagag	-378
-377	gaccggggagaggcctcccatggtcatggtcatggcagtacagaggccaggggccccggg	-318
-317	agggagggcgggcagtcaggagtgtgtggttctgtgctaggcttgtggacagcgcgcg	-258
-257	agcagctggggcaaggccggctccgtggctcgaggccgaggggtgcagctggacggccgc	-198
-197	agtcacagagacactgcagggagaagggcaggcagactgggggtgtgggagcaggcctgg	-138
-137	gccccatcggctatgagggcggggaagtggggcggggtggggagcctccgtggccctggcc	-78
-77	ccatctccagtccccagtcctggctcggacagatagggcgaggctgtgctgtcctttcag	-18
-17	aagacttcggcgccaccatggcatccagcatcctcaagtgggtgggtcagccaccagagct	42
1	M A S S I L K W V V S H Q S C	15
43	gcagcaggagcagcagaagcaagcccaggaccagagggaggaggccgggagcagcgacc	102
16	S R S S R S K P R D Q R E E A G S S D L	35
103	tgagcagcaggcaaggtgCGTggtggggccggggcagggcagtgccaggccaccagagctcgg	162
36	S S R Q G A L G R G R A V P G H Q S S G	55
163	ggcctccacaggggccctccc	183
56	P P Q G P S	61

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FIG. 8



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FIG. 9

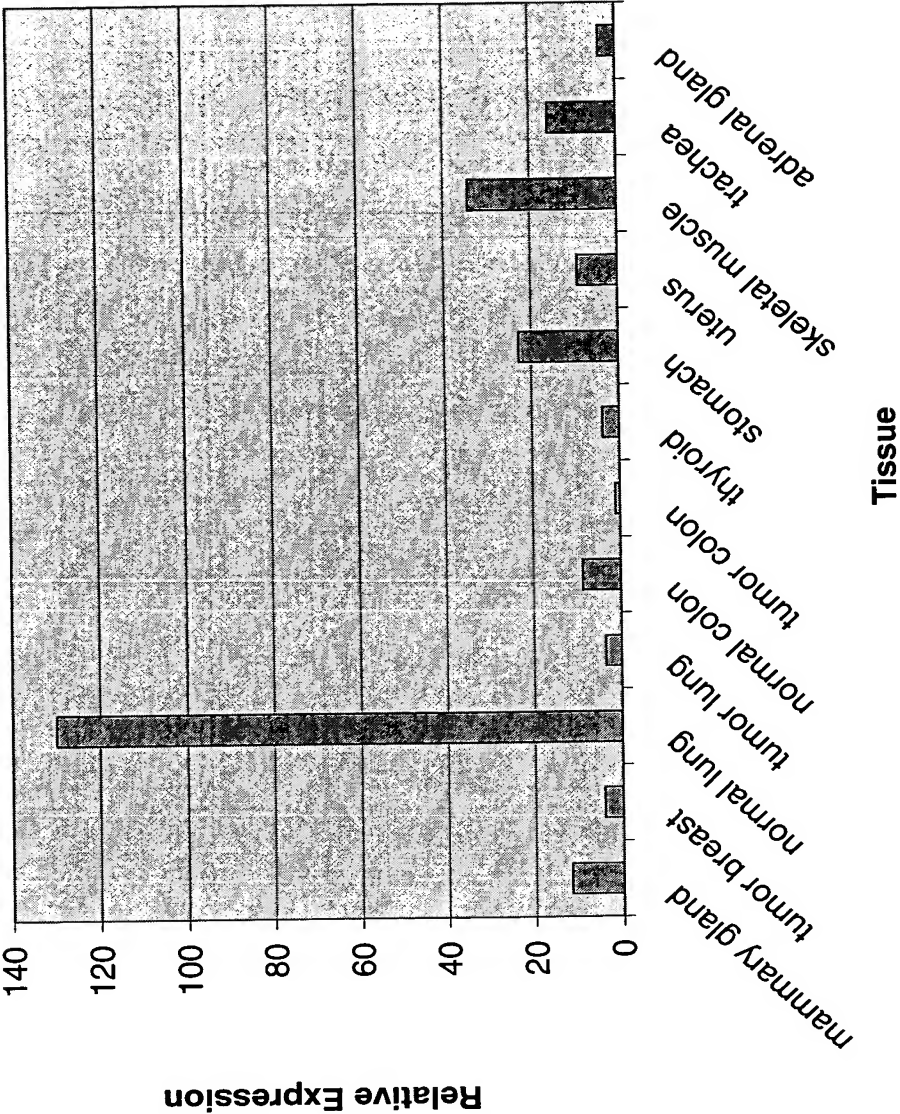


FIG. 10

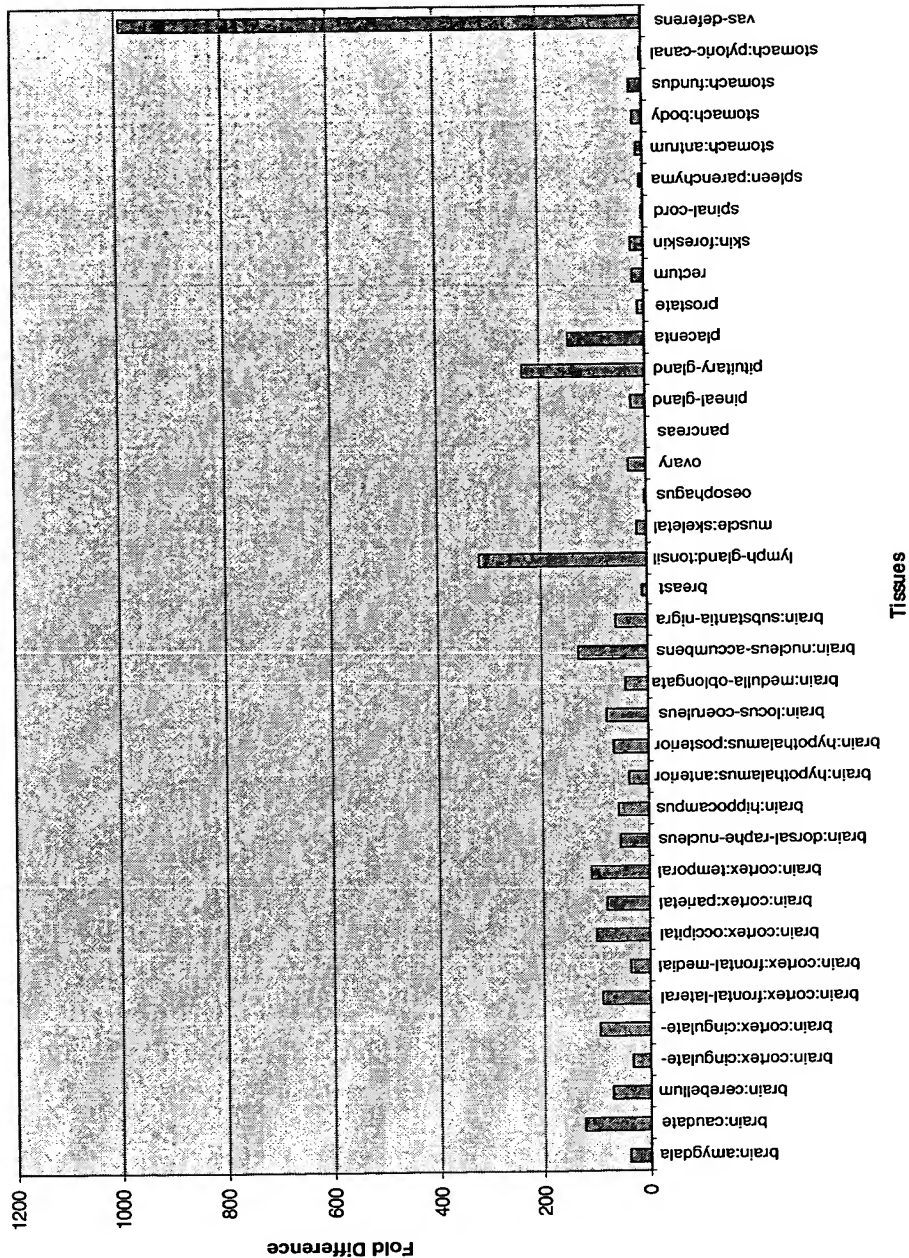


FIG. 11

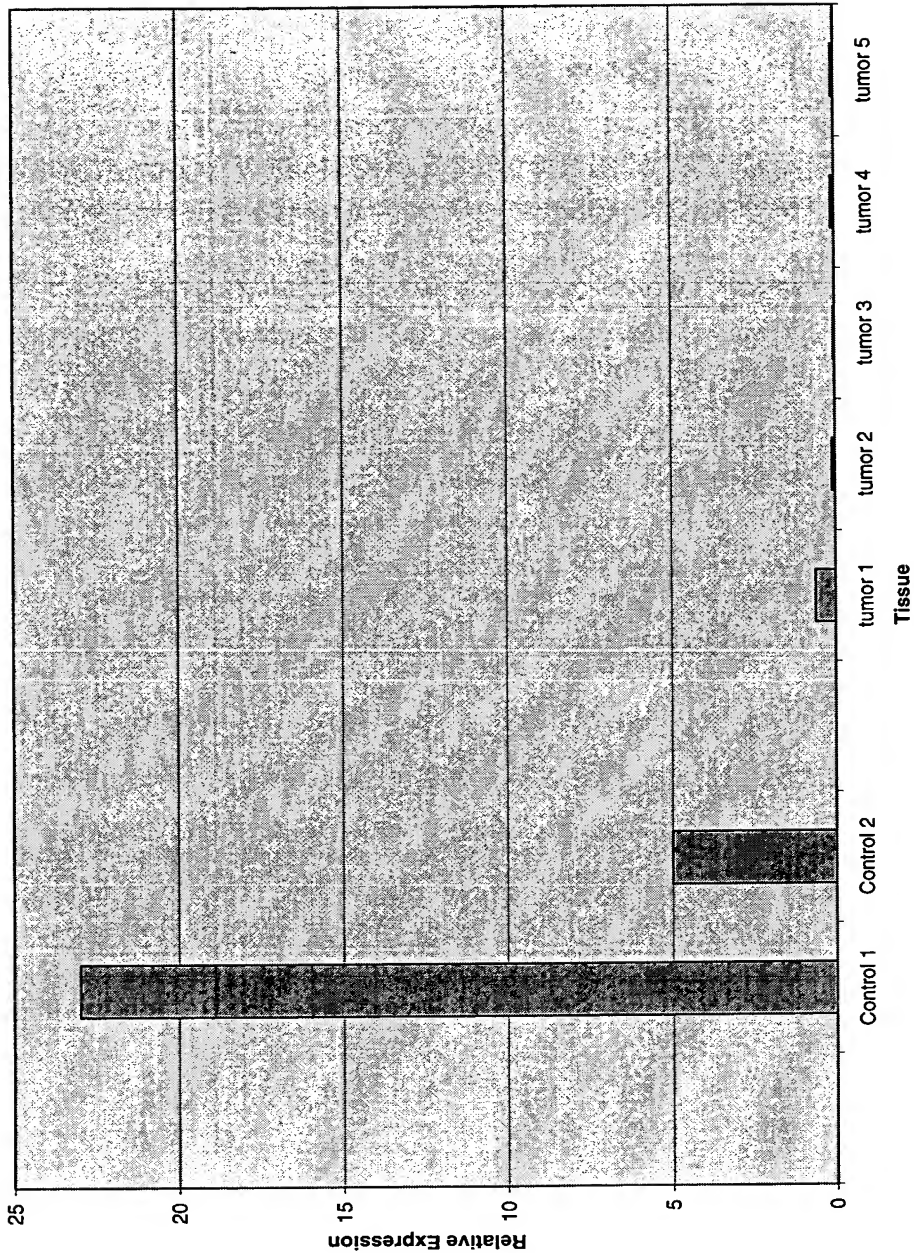


FIG. 12

Protein	Genbank ID	Identities	Similarities
Human HOTTTL protein	gi 6683745	57.5%	65.5%
Pig tubulin--tyrosine ligase protein (TTL)	gi 423218	29.4%	40.0%
Human tubulin tyrosine ligase-like protein (TTLH_HUMAN)	gi 20455371	53.3%	61.4%
Human tubulin tyrosine ligase-like protein (TTLL_HUMAN)	gi 20455347	27.4%	38.4%